Supplementary Materials for

Minfi: A flexible and comprehensive Bioconductor package for the analysis of Infinium DNA Methylation microarrays

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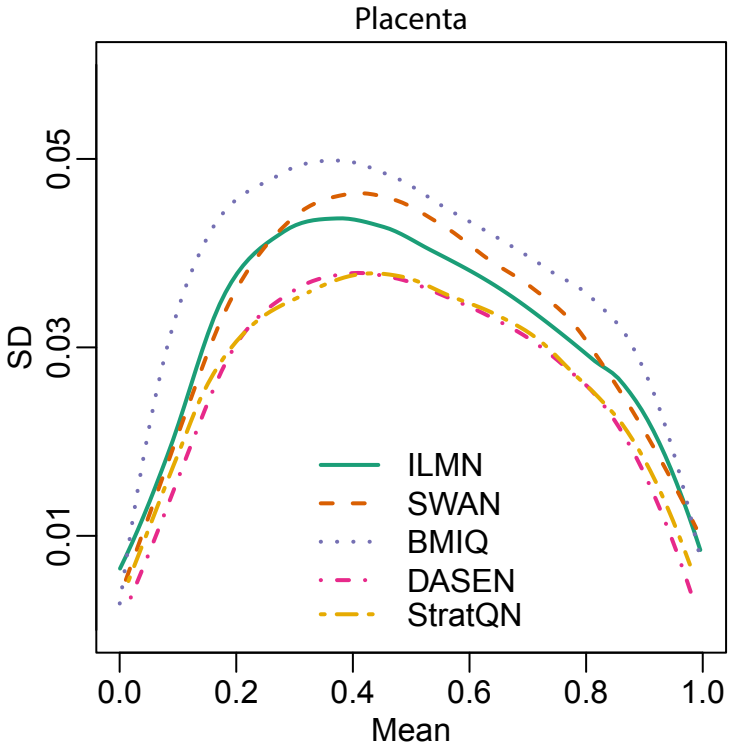
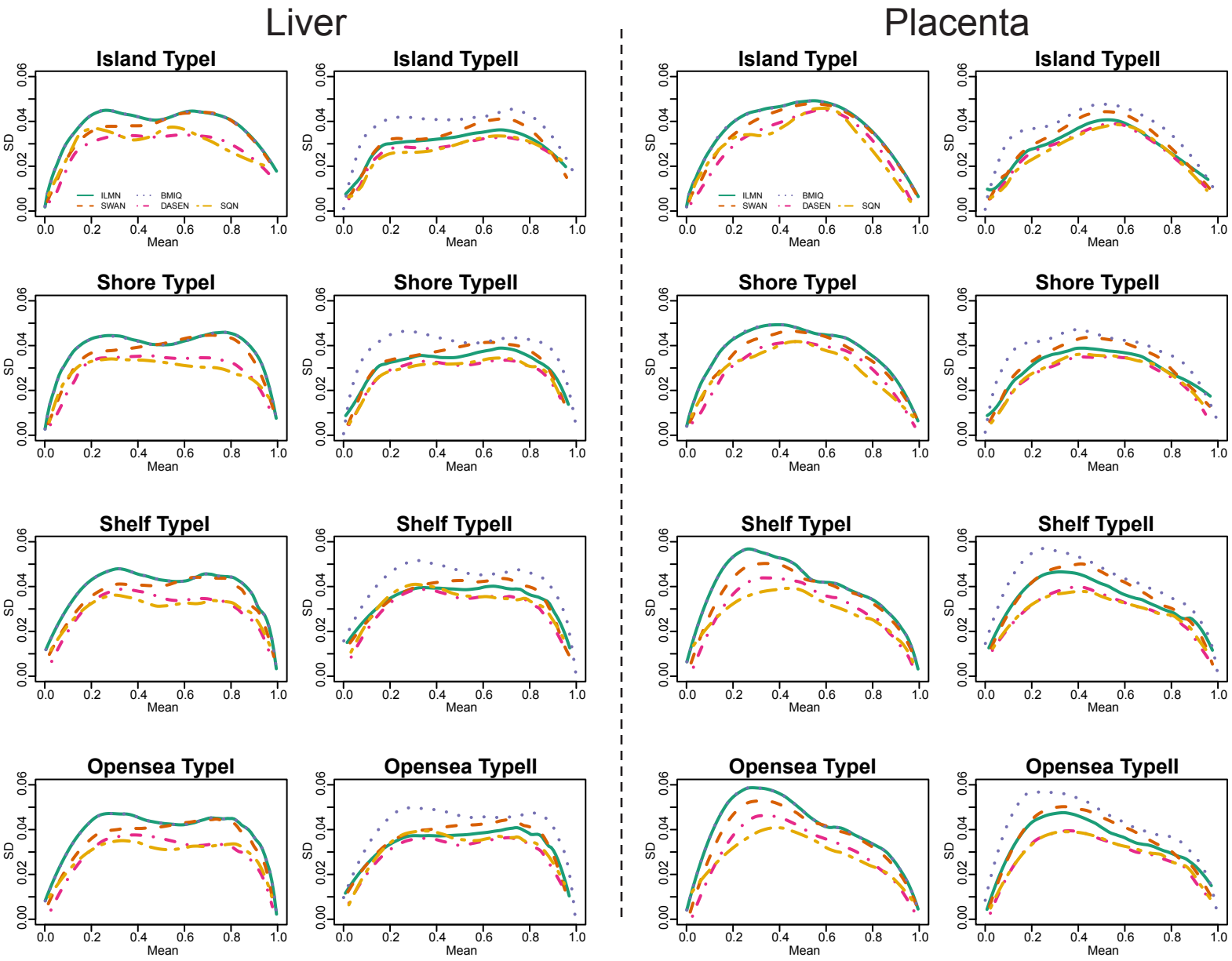
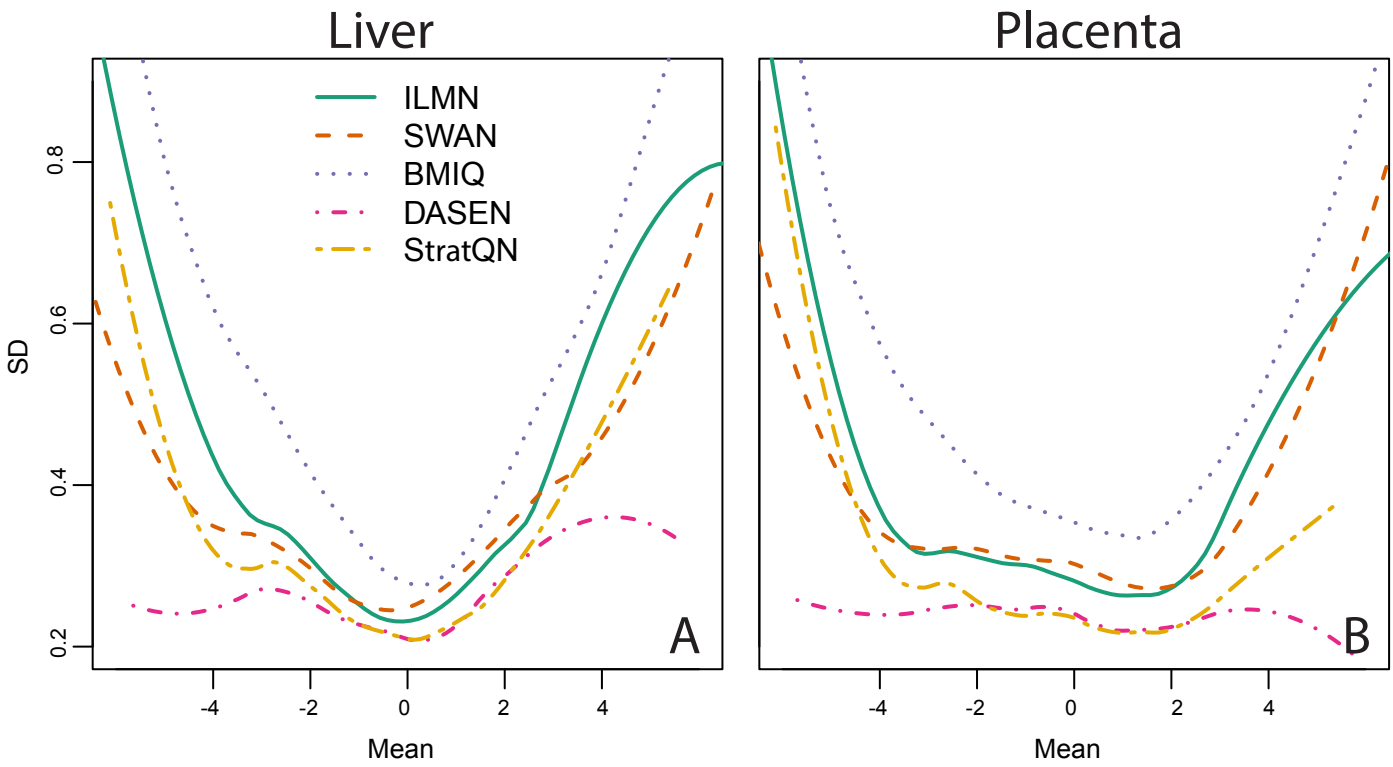


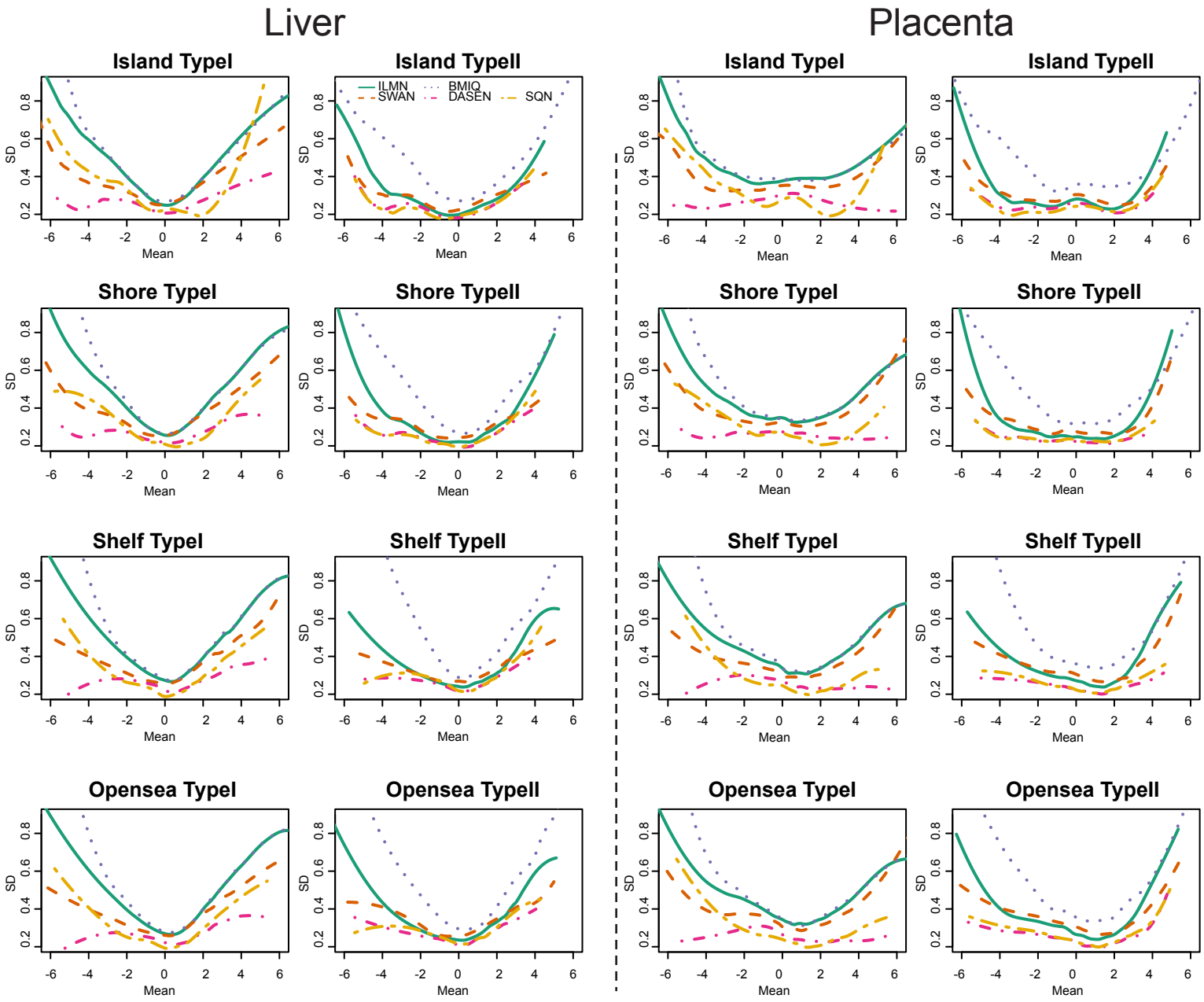
Supplementary Figure 1. As Figure 3A but for placenta replicates: for each locus we compute the average and standard deviation (SD) across placenta technical samples. We fit a loess curve to the SD versus average scatterplot for each method. The resulting curve is shown for each preprocessing method.



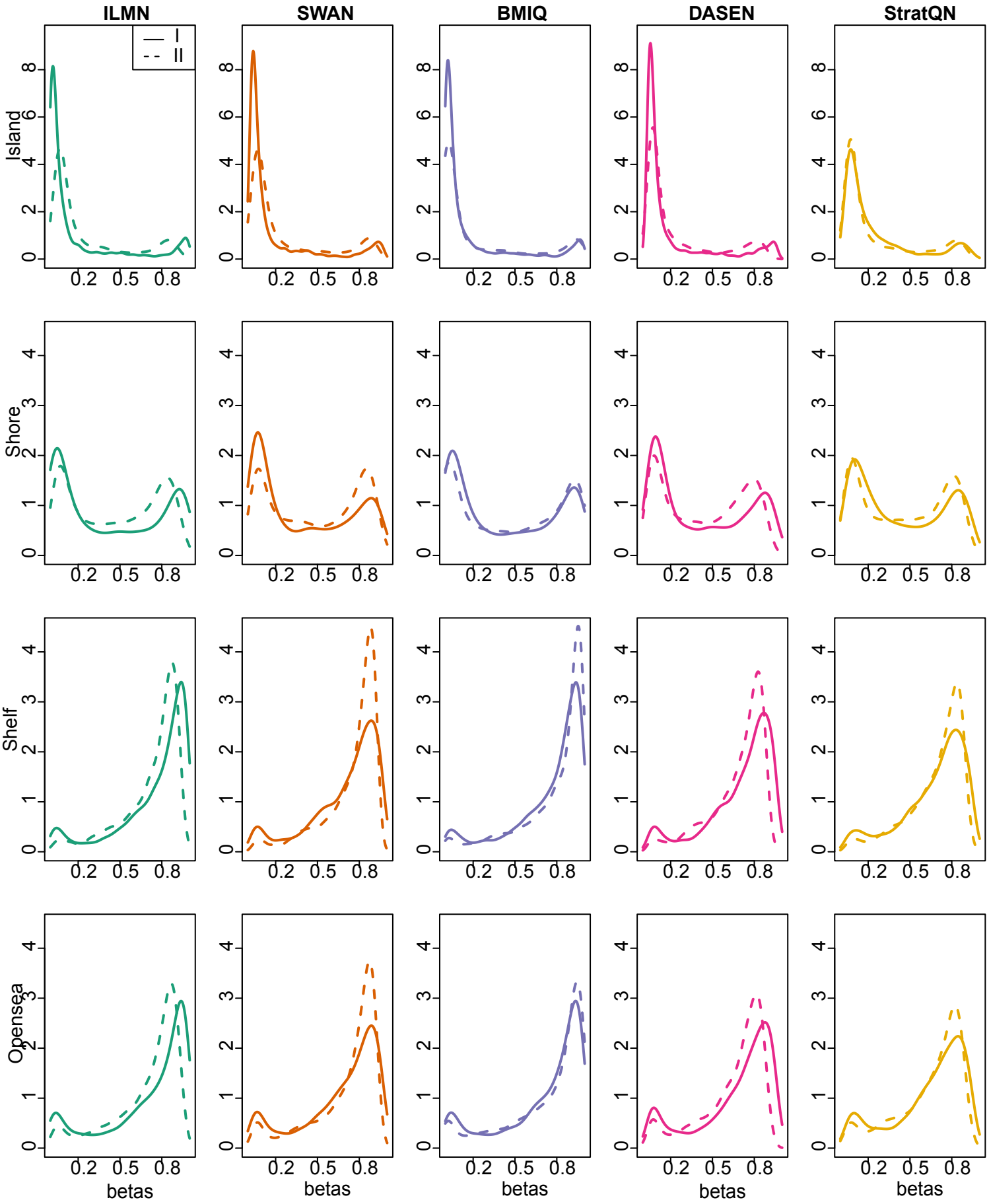
Supplementary Figure 2. As Supplementary Figure 1 but for both tissues and stratified by probe type and region: for each locus we compute the average and standard deviation (SD) across technical samples. We fit a loess curve to the SD versus average scatterplot for each method. The resulting curve is shown for each preprocessing method



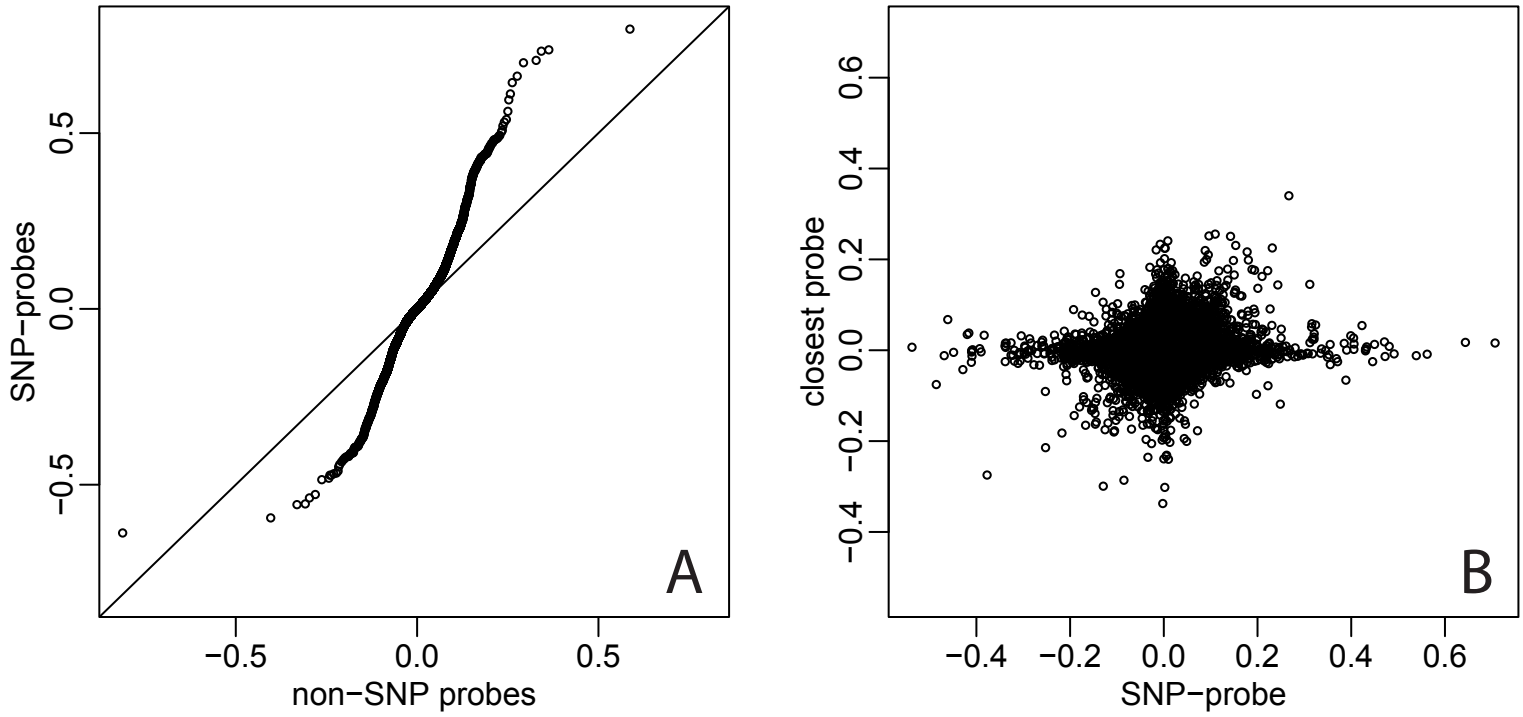
Supplementary Figure 3. As Supplementary Figure 1 but for the results of applying the algorithms to the data on the logit scale: for each locus we compute the average and standard deviation (SD) across technical samples. We fit a loess curve to the SD versus average scatterplot for each method. The resulting curve is shown for each preprocessing method.



Supplementary Figure 4. As Supplementary Figure 3 but stratified by probe type and region: for each locus we compute the average and standard deviation (SD) across technical samples. We fit a loess curve to the SD versus average scatterplot for each method. The resulting curve is shown for each preprocessing method.



Supplementary Figure 5. Distributions of beta methylation values stratified by probe type (Type I and II), genomic region, and preprocessing method.



Supplementary Figure 6. Genotype effects on DNA methylation levels. A) We computed the differences in average methylation between Caucasian and Hispanic ethnicities and plot a quantile-quantile plot of the SNP-affected probes versus the non-affected probes. B) Each SNP-affected probe is paired with its closest non-affected probe. We plot the Caucasian-Hispanic differences of the SNP affected probes against the difference at its closest non-affected probe.